SEQUENCE LISTING

<110> E. I. duPont de Nemours and Company, Inc.
Cheng, Qiong
Rouviere, Pierre
Tao, Luan

<120> Mutations Affecting Carotenoid Production

<130> CL-2028 US NA

<150> US 60/435612
<151> 2002-12-19

<160> 43

<170> PatentIn version 3.2

<210> 1
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<212> DNA
<213> Pantoea stewartii

<220>
<221> misc_feature
<222> (1)..(3)
<223> Alternative start code usage of TTG instead of ATG.

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ggtgccgcga tgcgtgaagg cacgctggca ccgggcaaac gtattcgtcc gatgctgctg 180

ttattaacag cgcgcgatct tggctgtgcg atcagtcacg ggggattact ggatttagcc 240

tgcgcggttg aaatggtgca tgctgcctcg ctgattctgg atgatatgcc ctgcatggac 300

gatgcgcaga tgcgtcgggg gcgtcccacc attcacacgc agtacggtga acatgtggcg 360

attctggcgg cggtcgcttt actcagcaaa gcgtttgggg tgattgccga ggctgaaggt 420

ctgacgccga tagccaaaac tcgcgcggtg tcggagctgt ccactgcgat tggcatgcag 480

ggtctggttc agggccagtt taaggacctc tcggaaggcg ataaaccccg cagcgccgat 540

gccatactgc taaccaatca gtttaaaacc agcacgctgt tttgcgcgtc aacgcaaatg 600

gcgtccattg cggccaacgc gtcctgcgaa gcgcgtgaga acctgcatcg tttctcgctc 660

gatctcggcc aggcctttca gttgcttgac gatcttaccg atggcatgac cgataccggc 720

aaagacatca atcaggatgc aggtaaatca acgctggtca atttattagg ctcaggcgcg 780

gtcgaagaac gcctgcgaca gcatttgcgc ctggccagtg aacacctttc cgcggcatgc 840

caaaacggcc attccaccac ccaacttttt attcaggcct ggtttgacaa aaaactcgct 900

gccgtcagtt aa 912

<210> 2
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<212> PRT
<213> Pantoea stewartii

<400> 2

Met Thr Val Cys Ala Lys Lys His Val His Leu Thr Gly Ile Ser Ala
1 5 10 15

Glu Gln Leu Leu Ala Asp Ile Asp Ser Arg Leu Asp Gln Leu Leu Pro
20 25 30

Val Gln Gly Glu Arg Asp Cys Val Gly Ala Ala Met Arg Glu Gly Thr
35 40 45

Leu Ala Pro Gly Lys Arg Ile Arg Pro Met Leu Leu Leu Leu Thr Ala
50 55 60

Arg Asp Leu Gly Cys Ala Ile Ser His Gly Gly Leu Leu Asp Leu Ala
65 70 75 80

Cys Ala Val Glu Met Val His Ala Ala Ser Leu Ile Leu Asp Asp Met
85 90 95

Pro Cys Met Asp Asp Ala Gln Met Arg Arg Gly Arg Pro Thr Ile His
100 105 110

Thr Gln Tyr Gly Glu His Val Ala Ile Leu Ala Ala Val Ala Leu Leu
115 120 125

Ser Lys Ala Phe Gly Val Ile Ala Glu Ala Glu Gly Leu Thr Pro Ile
130 135 140

Ala Lys Thr Arg Ala Val Ser Glu Leu Ser Thr Ala Ile Gly Met Gln
145 150 155 160

Gly Leu Val Gln Gly Gln Phe Lys Asp Leu Ser Glu Gly Asp Lys Pro
165 170 175

Arg Ser Ala Asp Ala Ile Leu Leu Thr Asn Gln Phe Lys Thr Ser Thr
180 185 190

Leu Phe Cys Ala Ser Thr Gln Met Ala Ser Ile Ala Ala Asn Ala Ser
195 200 205

Cys Glu Ala Arg Glu Asn Leu His Arg Phe Ser Leu Asp Leu Gly Gln
210 215 220

Ala Phe Gln Leu Leu Asp Asp Leu Thr Asp Gly Met Thr Asp Thr Gly
225 230 235 240

Lys Asp Ile Asn Gln Asp Ala Gly Lys Ser Thr Leu Val Asn Leu Leu
245 250 255

Gly Ser Gly Ala Val Glu Glu Arg Leu Arg Gln His Leu Arg Leu Ala
260 265 270

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Ser Glu His Leu Ser Ala Ala Cys Gln Asn Gly His Ser Thr Thr Gln
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Leu Phe Ile Gln Ala Trp Phe Asp Lys Lys Leu Ala Ala Val Ser
    290                 295                 300
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<210> 3
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Met Ser His Phe Ala Val Ile Ala Pro Pro Phe Phe Ser His Val Arg
1               5                   10                  15

gct ctg caa aac ctt gct cag gaa tta gtg gcc cgc ggt cat cgt gtt       96
Ala Leu Gln Asn Leu Ala Gln Glu Leu Val Ala Arg Gly His Arg Val
            20                  25                  30

acg ttt ttt cag caa cat gac tgc aaa gcg ctg gta acg ggc agc gat      144
Thr Phe Phe Gln Gln His Asp Cys Lys Ala Leu Val Thr Gly Ser Asp
        35                  40                  45

atc gga ttc cag acc gtc gga ctg caa acg cat cct ccc ggt tcc tta      192
Ile Gly Phe Gln Thr Val Gly Leu Gln Thr His Pro Pro Gly Ser Leu
    50                  55                  60

tcg cac ctg ctg cac ctg gcc gcg cac cca ctc gga ccc tcg atg tta      240
Ser His Leu Leu His Leu Ala Ala His Pro Leu Gly Pro Ser Met Leu
65                  70                  75                  80

cga ctg atc aat gaa atg gca cgt acc agc gat atg ctt tgc cgg gaa      288
Arg Leu Ile Asn Glu Met Ala Arg Thr Ser Asp Met Leu Cys Arg Glu
                85                  90                  95

ctg ccc gcc gct ttt cat gcg ttg cag ata gag ggc gtg atc gtt gat      336
Leu Pro Ala Ala Phe His Ala Leu Gln Ile Glu Gly Val Ile Val Asp
            100                 105                 110

caa atg gag ccg gca ggt gca gta gtc gca gaa gcg tca ggt ctg ccg      384
Gln Met Glu Pro Ala Gly Ala Val Val Ala Glu Ala Ser Gly Leu Pro
        115                 120                 125

ttt gtt tcg gtg gcc tgc gcg ctg ccg ctc aac cgc gaa ccg ggt ttg      432
Phe Val Ser Val Ala Cys Ala Leu Pro Leu Asn Arg Glu Pro Gly Leu
    130                 135                 140

cct ctg gcg gtg atg cct ttc gag tac ggc acc agc gat gcg gct cgg      480
Pro Leu Ala Val Met Pro Phe Glu Tyr Gly Thr Ser Asp Ala Ala Arg
145                 150                 155                 160

gaa cgc tat acc acc agc gaa aaa att tat gac tgg ctg atg cga cgt      528
Glu Arg Tyr Thr Thr Ser Glu Lys Ile Tyr Asp Trp Leu Met Arg Arg
                165                 170                 175

cac gat cgt gtg atc gcg cat cat gca tgc aga atg ggt tta gcc ccg      576
His Asp Arg Val Ile Ala His His Ala Cys Arg Met Gly Leu Ala Pro
            180                 185                 190
```

```
cgt gaa aaa ctg cat cat tgt ttt tct cca ctg gca caa atc agc cag      624
Arg Glu Lys Leu His His Cys Phe Ser Pro Leu Ala Gln Ile Ser Gln
        195                 200                 205

ttg atc ccc gaa ctg gat ttt ccc cgc aaa gcg ctg cca gac tgc ttt      672
Leu Ile Pro Glu Leu Asp Phe Pro Arg Lys Ala Leu Pro Asp Cys Phe
    210                 215                 220

cat gcg gtt gga ccg tta cgg caa ccc cag ggg acg ccg ggg tca tca      720
His Ala Val Gly Pro Leu Arg Gln Pro Gln Gly Thr Pro Gly Ser Ser
225                 230                 235                 240

act tct tat ttt ccg tcc ccg gac aaa ccc cgt att ttt gcc tcg ctg      768
Thr Ser Tyr Phe Pro Ser Pro Asp Lys Pro Arg Ile Phe Ala Ser Leu
                245                 250                 255

ggc acc ctg cag gga cat cgt tat ggc ctg ttc agg acc atc gcc aaa      816
Gly Thr Leu Gln Gly His Arg Tyr Gly Leu Phe Arg Thr Ile Ala Lys
            260                 265                 270

gcc tgc gaa gag gtg gat gcg cag tta ctg ttg gca cac tgt ggc ggc      864
Ala Cys Glu Glu Val Asp Ala Gln Leu Leu Leu Ala His Cys Gly Gly
        275                 280                 285

ctc tca gcc acg cag gca ggt gaa ctg gcc cgg ggc ggg gac att cag      912
Leu Ser Ala Thr Gln Ala Gly Glu Leu Ala Arg Gly Gly Asp Ile Gln
    290                 295                 300

gtt gtg gat ttt gcc gat caa tcc gca gca ctt tca cag gca cag ttg      960
Val Val Asp Phe Ala Asp Gln Ser Ala Ala Leu Ser Gln Ala Gln Leu
305                 310                 315                 320

aca atc aca cat ggt ggg atg aat acg gta ctg gac gct att gct tcc     1008
Thr Ile Thr His Gly Gly Met Asn Thr Val Leu Asp Ala Ile Ala Ser
                325                 330                 335

cgc aca ccg cta ctg gcg ctg ccg ctg gca ttt gat caa cct ggc gtg     1056
Arg Thr Pro Leu Leu Ala Leu Pro Leu Ala Phe Asp Gln Pro Gly Val
            340                 345                 350

gca tca cga att gtt tat cat ggc atc ggc aag cgt gcg tct cgg ttt     1104
Ala Ser Arg Ile Val Tyr His Gly Ile Gly Lys Arg Ala Ser Arg Phe
        355                 360                 365

act acc agc cat gcg ctg gcg cgg cag att cga tcg ctg ctg act aac     1152
Thr Thr Ser His Ala Leu Ala Arg Gln Ile Arg Ser Leu Leu Thr Asn
    370                 375                 380

acc gat tac ccg cag cgt atg aca aaa att cag gcc gca ttg cgt ctg     1200
Thr Asp Tyr Pro Gln Arg Met Thr Lys Ile Gln Ala Ala Leu Arg Leu
385                 390                 395                 400

gca ggc ggc aca cca gcc gcc gcc gat att gtt gaa cag gcg atg cgg     1248
Ala Gly Gly Thr Pro Ala Ala Ala Asp Ile Val Glu Gln Ala Met Arg
                405                 410                 415

acc tgt cag cca gta ctc agt ggg cag gat tat gca acc gca cta tga     1296
Thr Cys Gln Pro Val Leu Ser Gly Gln Asp Tyr Ala Thr Ala Leu
            420                 425                 430
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<210> 4
<211> 431
<212> PRT
<213> Pantoea stewartii

<400> 4

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Met Ser His Phe Ala Val Ile Ala Pro Pro Phe Phe Ser His Val Arg
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Ala Leu Gln Asn Leu Ala Gln Glu Leu Val Ala Arg Gly His Arg Val
            20                  25                  30

Thr Phe Phe Gln Gln His Asp Cys Lys Ala Leu Val Thr Gly Ser Asp
        35                  40                  45

Ile Gly Phe Gln Thr Val Gly Leu Gln Thr His Pro Pro Gly Ser Leu
    50                  55                  60

Ser His Leu Leu His Leu Ala Ala His Pro Leu Gly Pro Ser Met Leu
65                  70                  75                  80

Arg Leu Ile Asn Glu Met Ala Arg Thr Ser Asp Met Leu Cys Arg Glu
                85                  90                  95

Leu Pro Ala Ala Phe His Ala Leu Gln Ile Glu Gly Val Ile Val Asp
            100                 105                 110

Gln Met Glu Pro Ala Gly Ala Val Val Ala Glu Ala Ser Gly Leu Pro
        115                 120                 125

Phe Val Ser Val Ala Cys Ala Leu Pro Leu Asn Arg Glu Pro Gly Leu
    130                 135                 140

Pro Leu Ala Val Met Pro Phe Glu Tyr Gly Thr Ser Asp Ala Ala Arg
145                 150                 155                 160

Glu Arg Tyr Thr Thr Ser Glu Lys Ile Tyr Asp Trp Leu Met Arg Arg
                165                 170                 175

His Asp Arg Val Ile Ala His His Ala Cys Arg Met Gly Leu Ala Pro
            180                 185                 190

Arg Glu Lys Leu His His Cys Phe Ser Pro Leu Ala Gln Ile Ser Gln
        195                 200                 205

Leu Ile Pro Glu Leu Asp Phe Pro Arg Lys Ala Leu Pro Asp Cys Phe
    210                 215                 220

His Ala Val Gly Pro Leu Arg Gln Pro Gln Gly Thr Pro Gly Ser Ser
225                 230                 235                 240

Thr Ser Tyr Phe Pro Ser Pro Asp Lys Pro Arg Ile Phe Ala Ser Leu
                245                 250                 255

Gly Thr Leu Gln Gly His Arg Tyr Gly Leu Phe Arg Thr Ile Ala Lys
            260                 265                 270
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Ala Cys Glu Glu Val Asp Ala Gln Leu Leu Leu Ala His Cys Gly Gly
        275                 280                 285

Leu Ser Ala Thr Gln Ala Gly Glu Leu Ala Arg Gly Gly Asp Ile Gln
    290                 295                 300

Val Val Asp Phe Ala Asp Gln Ser Ala Ala Leu Ser Gln Ala Gln Leu
305                 310                 315                 320

Thr Ile Thr His Gly Gly Met Asn Thr Val Leu Asp Ala Ile Ala Ser
                325                 330                 335

Arg Thr Pro Leu Leu Ala Leu Pro Leu Ala Phe Asp Gln Pro Gly Val
            340                 345                 350

Ala Ser Arg Ile Val Tyr His Gly Ile Gly Lys Arg Ala Ser Arg Phe
        355                 360                 365

Thr Thr Ser His Ala Leu Ala Arg Gln Ile Arg Ser Leu Leu Thr Asn
    370                 375                 380

Thr Asp Tyr Pro Gln Arg Met Thr Lys Ile Gln Ala Ala Leu Arg Leu
385                 390                 395                 400

Ala Gly Gly Thr Pro Ala Ala Ala Asp Ile Val Glu Gln Ala Met Arg
                405                 410                 415

Thr Cys Gln Pro Val Leu Ser Gly Gln Asp Tyr Ala Thr Ala Leu
            420                 425                 430


<210>  5
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<212>  DNA
<213>  Pantoea stewartii


<220>
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<222>  (1)..(1149)

<400>  5
atg caa ccg cac tat gat ctc att ctg gtc ggt gcc ggt ctg gct aat       48
Met Gln Pro His Tyr Asp Leu Ile Leu Val Gly Ala Gly Leu Ala Asn
1               5                   10                  15

ggc ctt atc gcg ctc cgg ctt cag caa cag cat ccg gat atg cgg atc       96
Gly Leu Ile Ala Leu Arg Leu Gln Gln His Pro Asp Met Arg Ile
            20                  25                  30

ttg ctt att gag gcg ggt cct gag gcg gga ggg aac cat acc tgg tcc      144
Leu Leu Ile Glu Ala Gly Pro Glu Ala Gly Gly Asn His Thr Trp Ser
        35                  40                  45

ttt cac gaa gag gat tta acg ctg aat cag cat cgc tgg ata gcg ccg      192
Phe His Glu Glu Asp Leu Thr Leu Asn Gln His Arg Trp Ile Ala Pro
    50                  55                  60
```

```
ctt gtg gtc cat cac tgg ccc gac tac cag gtt cgt ttc ccc caa cgc      240
Leu Val Val His His Trp Pro Asp Tyr Gln Val Arg Phe Pro Gln Arg
65                  70                  75                  80

cgt cgc cat gtg aac agt ggc tac tac tgc gtg acc tcc cgg cat ttc      288
Arg Arg His Val Asn Ser Gly Tyr Tyr Cys Val Thr Ser Arg His Phe
                85                  90                  95

gcc ggg ata ctc cgg caa cag ttt gga caa cat tta tgg ctg cat acc      336
Ala Gly Ile Leu Arg Gln Gln Phe Gly Gln His Leu Trp Leu His Thr
            100                 105                 110

gcg gtt tca gcc gtt cat gct gaa tcg gtc cag tta gcg gat ggc cgg      384
Ala Val Ser Ala Val His Ala Glu Ser Val Gln Leu Ala Asp Gly Arg
        115                 120                 125

att att cat gcc agt aca gtg atc gac gga cgg ggt tac acg cct gat      432
Ile Ile His Ala Ser Thr Val Ile Asp Gly Arg Gly Tyr Thr Pro Asp
    130                 135                 140

tct gca cta cgc gta gga ttc cag gca ttt atc ggt cag gag tgg caa      480
Ser Ala Leu Arg Val Gly Phe Gln Ala Phe Ile Gly Gln Glu Trp Gln
145                 150                 155                 160

ctg agc gcg ccg cat ggt tta tcg tca ccg att atc atg gat gcg acg      528
Leu Ser Ala Pro His Gly Leu Ser Ser Pro Ile Ile Met Asp Ala Thr
                165                 170                 175

gtc gat cag caa aat ggc tac cgc ttt gtt tat acc ctg ccg ctt tcc      576
Val Asp Gln Gln Asn Gly Tyr Arg Phe Val Tyr Thr Leu Pro Leu Ser
            180                 185                 190

gca acc gca ctg ctg atc gaa gac aca cac tac att gac aag gct aat      624
Ala Thr Ala Leu Leu Ile Glu Asp Thr His Tyr Ile Asp Lys Ala Asn
        195                 200                 205

ctt cag gcc gaa cgg gcg cgt cag aac att cgc gat tat gct gcg cga      672
Leu Gln Ala Glu Arg Ala Arg Gln Asn Ile Arg Asp Tyr Ala Ala Arg
    210                 215                 220

cag ggt tgg ccg tta cag acg ttg ctg cgg gaa gaa cag ggt gca ttg      720
Gln Gly Trp Pro Leu Gln Thr Leu Leu Arg Glu Glu Gln Gly Ala Leu
225                 230                 235                 240

ccc att acg tta acg ggc gat aat cgt cag ttt tgg caa cag caa ccg      768
Pro Ile Thr Leu Thr Gly Asp Asn Arg Gln Phe Trp Gln Gln Gln Pro
                245                 250                 255

caa gcc tgt agc gga tta cgc gcc ggg ctg ttt cat ccg aca acc ggc      816
Gln Ala Cys Ser Gly Leu Arg Ala Gly Leu Phe His Pro Thr Thr Gly
            260                 265                 270

tac tcc cta ccg ctc gcg gtg gcg ctg gcc gat cgt ctc agc gcg ctg      864
Tyr Ser Leu Pro Leu Ala Val Ala Leu Ala Asp Arg Leu Ser Ala Leu
        275                 280                 285

gat gtg ttt acc tct tcc tct gtt cac cag acg att gct cac ttt gcc      912
Asp Val Phe Thr Ser Ser Ser Val His Gln Thr Ile Ala His Phe Ala
    290                 295                 300

cag caa cgt tgg cag caa cag ggg ttt ttc cgc atg ctg aat cgc atg      960
Gln Gln Arg Trp Gln Gln Gln Gly Phe Phe Arg Met Leu Asn Arg Met
305                 310                 315                 320

ttg ttt tta gcc gga ccg gcc gag tca cgc tgg cgt gtg atg cag cgt     1008
Leu Phe Leu Ala Gly Pro Ala Glu Ser Arg Trp Arg Val Met Gln Arg
                325                 330                 335
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```
ttc tat ggc tta ccc gag gat ttg att gcc cgc ttt tat gcg gga aaa      1056
Phe Tyr Gly Leu Pro Glu Asp Leu Ile Ala Arg Phe Tyr Ala Gly Lys
            340                 345                 350

ctc acc gtg acc gat cgg cta cgc att ctg agc ggc aag ccg ccc gtt      1104
Leu Thr Val Thr Asp Arg Leu Arg Ile Leu Ser Gly Lys Pro Pro Val
        355                 360                 365

ccc gtt ttc gcg gca ttg cag gca att atg acg act cat cgt tga          1149
Pro Val Phe Ala Ala Leu Gln Ala Ile Met Thr Thr His Arg
    370                 375                 380


<210>  6
<211>  382
<212>  PRT
<213>  Pantoea stewartii

<400>  6

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Gly Leu Ile Ala Leu Arg Leu Gln Gln Gln His Pro Asp Met Arg Ile
            20                  25                  30


Leu Leu Ile Glu Ala Gly Pro Glu Ala Gly Gly Asn His Thr Trp Ser
        35                  40                  45


Phe His Glu Glu Asp Leu Thr Leu Asn Gln His Arg Trp Ile Ala Pro
    50                  55                  60


Leu Val Val His His Trp Pro Asp Tyr Gln Val Arg Phe Pro Gln Arg
65                  70                  75                  80


Arg Arg His Val Asn Ser Gly Tyr Tyr Cys Val Thr Ser Arg His Phe
                85                  90                  95


Ala Gly Ile Leu Arg Gln Gln Phe Gly Gln His Leu Trp Leu His Thr
            100                 105                 110


Ala Val Ser Ala Val His Ala Glu Ser Val Gln Leu Ala Asp Gly Arg
        115                 120                 125


Ile Ile His Ala Ser Thr Val Ile Asp Gly Arg Gly Tyr Thr Pro Asp
    130                 135                 140


Ser Ala Leu Arg Val Gly Phe Gln Ala Phe Ile Gly Gln Glu Trp Gln
145                 150                 155                 160


Leu Ser Ala Pro His Gly Leu Ser Ser Pro Ile Ile Met Asp Ala Thr
                165                 170                 175


Val Asp Gln Gln Asn Gly Tyr Arg Phe Val Tyr Thr Leu Pro Leu Ser
            180                 185                 190
```

```
Ala Thr Ala Leu Leu Ile Glu Asp Thr His Tyr Ile Asp Lys Ala Asn
        195                 200                 205

Leu Gln Ala Glu Arg Ala Arg Gln Asn Ile Arg Asp Tyr Ala Ala Arg
    210                 215                 220

Gln Gly Trp Pro Leu Gln Thr Leu Leu Arg Glu Glu Gln Gly Ala Leu
225                 230                 235                 240

Pro Ile Thr Leu Thr Gly Asp Asn Arg Gln Phe Trp Gln Gln Gln Pro
                245                 250                 255

Gln Ala Cys Ser Gly Leu Arg Ala Gly Leu Phe His Pro Thr Thr Gly
            260                 265                 270

Tyr Ser Leu Pro Leu Ala Val Ala Leu Ala Asp Arg Leu Ser Ala Leu
        275                 280                 285

Asp Val Phe Thr Ser Ser Ser Val His Gln Thr Ile Ala His Phe Ala
    290                 295                 300

Gln Gln Arg Trp Gln Gln Gln Gly Phe Phe Arg Met Leu Asn Arg Met
305                 310                 315                 320

Leu Phe Leu Ala Gly Pro Ala Glu Ser Arg Trp Arg Val Met Gln Arg
                325                 330                 335

Phe Tyr Gly Leu Pro Glu Asp Leu Ile Ala Arg Phe Tyr Ala Gly Lys
            340                 345                 350

Leu Thr Val Thr Asp Arg Leu Arg Ile Leu Ser Gly Lys Pro Pro Val
        355                 360                 365

Pro Val Phe Ala Ala Leu Gln Ala Ile Met Thr Thr His Arg
    370                 375                 380
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<210> 7
<211> 1479
<212> DNA
<213> Pantoea stewartii

<220>
<221> CDS
<222> (1)..(1479)

<400> 7

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Met Lys Pro Thr Thr Val Ile Gly Ala Gly Phe Gly Gly Leu Ala Leu
1               5                   10                  15

gca att cgt tta cag gcc gca ggt att cct gtt ttg ctg ctt gag cag       96
Ala Ile Arg Leu Gln Ala Ala Gly Ile Pro Val Leu Leu Leu Glu Gln
            20                  25                  30

cgc gac aag ccg ggt ggc cgg gct tat gtt tat cag gag cag ggc ttt      144
```

```
Arg Asp Lys Pro Gly Gly Arg Ala Tyr Val Tyr Gln Glu Gln Gly Phe
        35                  40                  45

act ttt gat gca ggc cct acc gtt atc acc gat ccc agc gcg att gaa      192
Thr Phe Asp Ala Gly Pro Thr Val Ile Thr Asp Pro Ser Ala Ile Glu
    50                  55                  60

gaa ctg ttt gct ctg gcc ggt aaa cag ctt aag gat tac gtc gag ctg      240
Glu Leu Phe Ala Leu Ala Gly Lys Gln Leu Lys Asp Tyr Val Glu Leu
65                  70                  75                  80

ttg ccg gtc acg ccg ttt tat cgc ctg tgc tgg gag tcc ggc aag gtc      288
Leu Pro Val Thr Pro Phe Tyr Arg Leu Cys Trp Glu Ser Gly Lys Val
                85                  90                  95

ttc aat tac gat aac gac cag gcc cag tta gaa gcg cag ata cag cag      336
Phe Asn Tyr Asp Asn Asp Gln Ala Gln Leu Glu Ala Gln Ile Gln Gln
            100                 105                 110

ttt aat ccg cgc gat gtt gcg ggt tat cga gcg ttc ctt gac tat tcg      384
Phe Asn Pro Arg Asp Val Ala Gly Tyr Arg Ala Phe Leu Asp Tyr Ser
        115                 120                 125

cgt gcc gta ttc aat gag ggc tat ctg aag ctc ggc act gtg cct ttt      432
Arg Ala Val Phe Asn Glu Gly Tyr Leu Lys Leu Gly Thr Val Pro Phe
    130                 135                 140

tta tcg ttc aaa gac atg ctt cgg gcc gcg ccc cag ttg gca aag ctg      480
Leu Ser Phe Lys Asp Met Leu Arg Ala Ala Pro Gln Leu Ala Lys Leu
145                 150                 155                 160

cag gca tgg cgc agc gtt tac agt aaa gtt gcc ggc tac att gag gat      528
Gln Ala Trp Arg Ser Val Tyr Ser Lys Val Ala Gly Tyr Ile Glu Asp
                165                 170                 175

gag cat ctt cgg cag gcg ttt tct ttt cac tcg ctc tta gtg ggg ggg      576
Glu His Leu Arg Gln Ala Phe Ser Phe His Ser Leu Leu Val Gly Gly
            180                 185                 190

aat ccg ttt gca acc tcg tcc att tat acg ctg att cac gcg tta gaa      624
Asn Pro Phe Ala Thr Ser Ser Ile Tyr Thr Leu Ile His Ala Leu Glu
        195                 200                 205

cgg gaa tgg ggc gtc tgg ttt cca cgc ggt gga acc ggt gcg ctg gtc      672
Arg Glu Trp Gly Val Trp Phe Pro Arg Gly Gly Thr Gly Ala Leu Val
    210                 215                 220

aat ggc atg atc aag ctg ttt cag gat ctg ggc ggc gaa gtc gtg ctt      720
Asn Gly Met Ile Lys Leu Phe Gln Asp Leu Gly Gly Glu Val Val Leu
225                 230                 235                 240

aac gcc cgg gtc agt cat atg gaa acc gtt ggg gac aag att cag gcc      768
Asn Ala Arg Val Ser His Met Glu Thr Val Gly Asp Lys Ile Gln Ala
                245                 250                 255

gtg cag ttg gaa gac ggc aga cgg ttt gaa acc tgc gcg gtg gcg tcg      816
Val Gln Leu Glu Asp Gly Arg Arg Phe Glu Thr Cys Ala Val Ala Ser
            260                 265                 270

aac gct gat gtt gta cat acc tat cgc gat ctg ctg tct cag cat ccc      864
Asn Ala Asp Val Val His Thr Tyr Arg Asp Leu Leu Ser Gln His Pro
        275                 280                 285

gca gcc gct aag cag gcg aaa aaa ctg caa tcc aag cgt atg agt aac      912
Ala Ala Ala Lys Gln Ala Lys Lys Leu Gln Ser Lys Arg Met Ser Asn
    290                 295                 300

tca ctg ttt gta ctc tat ttt ggt ctc aac cat cat cac gat caa ctc      960
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```
Ser Leu Phe Val Leu Tyr Phe Gly Leu Asn His His His Asp Gln Leu
305                 310                 315                 320

gcc cat cat acc gtc tgt ttt ggg cca cgc tac cgt gaa ctg att cac     1008
Ala His His Thr Val Cys Phe Gly Pro Arg Tyr Arg Glu Leu Ile His
                325                 330                 335

gaa att ttt aac cat gat ggt ctg gct gag gat ttt tcg ctt tat tta     1056
Glu Ile Phe Asn His Asp Gly Leu Ala Glu Asp Phe Ser Leu Tyr Leu
            340                 345                 350

cac gca cct tgt gtc acg gat ccg tca ctg gca ccg gaa ggg tgc ggc     1104
His Ala Pro Cys Val Thr Asp Pro Ser Leu Ala Pro Glu Gly Cys Gly
        355                 360                 365

agc tat tat gtg ctg gcg cct gtt cca cac tta ggc acg gcg aac ctc     1152
Ser Tyr Tyr Val Leu Ala Pro Val Pro His Leu Gly Thr Ala Asn Leu
    370                 375                 380

gac tgg gcg gta gaa gga ccc cga ctg cgc gat cgt att ttt gac tac     1200
Asp Trp Ala Val Glu Gly Pro Arg Leu Arg Asp Arg Ile Phe Asp Tyr
385                 390                 395                 400

ctt gag caa cat tac atg cct ggc ttg cga agc cag ttg gtg acg cac     1248
Leu Glu Gln His Tyr Met Pro Gly Leu Arg Ser Gln Leu Val Thr His
                405                 410                 415

cgt atg ttt acg ccg ttc gat ttc cgc gac gag ctc aat gcc tgg caa     1296
Arg Met Phe Thr Pro Phe Asp Phe Arg Asp Glu Leu Asn Ala Trp Gln
            420                 425                 430

ggt tcg gcc ttc tcg gtt gaa cct att ctg acc cag agc gcc tgg ttc     1344
Gly Ser Ala Phe Ser Val Glu Pro Ile Leu Thr Gln Ser Ala Trp Phe
        435                 440                 445

cga cca cat aac cgc gat aag cac att gat aat ctt tat ctg gtt ggc     1392
Arg Pro His Asn Arg Asp Lys His Ile Asp Asn Leu Tyr Leu Val Gly
    450                 455                 460

gca ggc acc cat cct ggc gcg ggc att ccc ggc gta atc ggc tcg gcg     1440
Ala Gly Thr His Pro Gly Ala Gly Ile Pro Gly Val Ile Gly Ser Ala
465                 470                 475                 480

aag gcg acg gca ggc tta atg ctg gag gac ctg att tga                 1479
Lys Ala Thr Ala Gly Leu Met Leu Glu Asp Leu Ile
                485                 490
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<210> 8
<211> 492
<212> PRT
<213> Pantoea stewartii

<400> 8

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Met Lys Pro Thr Thr Val Ile Gly Ala Gly Phe Gly Gly Leu Ala Leu
1               5                   10                  15

Ala Ile Arg Leu Gln Ala Ala Gly Ile Pro Val Leu Leu Leu Glu Gln
            20                  25                  30

Arg Asp Lys Pro Gly Gly Arg Ala Tyr Val Tyr Gln Glu Gln Gly Phe
        35                  40                  45

Thr Phe Asp Ala Gly Pro Thr Val Ile Thr Asp Pro Ser Ala Ile Glu
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50 55 60

Glu Leu Phe Ala Leu Ala Gly Lys Gln Leu Lys Asp Tyr Val Glu Leu
65 70 75 80

Leu Pro Val Thr Pro Phe Tyr Arg Leu Cys Trp Glu Ser Gly Lys Val
85 90 95

Phe Asn Tyr Asp Asn Asp Gln Ala Gln Leu Glu Ala Gln Ile Gln Gln
100 105 110

Phe Asn Pro Arg Asp Val Ala Gly Tyr Arg Ala Phe Leu Asp Tyr Ser
115 120 125

Arg Ala Val Phe Asn Glu Gly Tyr Leu Lys Leu Gly Thr Val Pro Phe
130 135 140

Leu Ser Phe Lys Asp Met Leu Arg Ala Ala Pro Gln Leu Ala Lys Leu
145 150 155 160

Gln Ala Trp Arg Ser Val Tyr Ser Lys Val Ala Gly Tyr Ile Glu Asp
165 170 175

Glu His Leu Arg Gln Ala Phe Ser Phe His Ser Leu Leu Val Gly Gly
180 185 190

Asn Pro Phe Ala Thr Ser Ser Ile Tyr Thr Leu Ile His Ala Leu Glu
195 200 205

Arg Glu Trp Gly Val Trp Phe Pro Arg Gly Gly Thr Gly Ala Leu Val
210 215 220

Asn Gly Met Ile Lys Leu Phe Gln Asp Leu Gly Gly Glu Val Val Leu
225 230 235 240

Asn Ala Arg Val Ser His Met Glu Thr Val Gly Asp Lys Ile Gln Ala
245 250 255

Val Gln Leu Glu Asp Gly Arg Arg Phe Glu Thr Cys Ala Val Ala Ser
260 265 270

Asn Ala Asp Val Val His Thr Tyr Arg Asp Leu Leu Ser Gln His Pro
275 280 285

Ala Ala Ala Lys Gln Ala Lys Lys Leu Gln Ser Lys Arg Met Ser Asn
290 295 300

Ser Leu Phe Val Leu Tyr Phe Gly Leu Asn His His His Asp Gln Leu
305 310 315 320

Ala His His Thr Val Cys Phe Gly Pro Arg Tyr Arg Glu Leu Ile His

325 330 335

Glu Ile Phe Asn His Asp Gly Leu Ala Glu Asp Phe Ser Leu Tyr Leu
340 345 350

His Ala Pro Cys Val Thr Asp Pro Ser Leu Ala Pro Glu Gly Cys Gly
355 360 365

Ser Tyr Tyr Val Leu Ala Pro Val Pro His Leu Gly Thr Ala Asn Leu
370 375 380

Asp Trp Ala Val Glu Gly Pro Arg Leu Arg Asp Arg Ile Phe Asp Tyr
385 390 395 400

Leu Glu Gln His Tyr Met Pro Gly Leu Arg Ser Gln Leu Val Thr His
405 410 415

Arg Met Phe Thr Pro Phe Asp Phe Arg Asp Glu Leu Asn Ala Trp Gln
420 425 430

Gly Ser Ala Phe Ser Val Glu Pro Ile Leu Thr Gln Ser Ala Trp Phe
435 440 445

Arg Pro His Asn Arg Asp Lys His Ile Asp Asn Leu Tyr Leu Val Gly
450 455 460

Ala Gly Thr His Pro Gly Ala Gly Ile Pro Gly Val Ile Gly Ser Ala
465 470 475 480

Lys Ala Thr Ala Gly Leu Met Leu Glu Asp Leu Ile
485 490

<210> 9
<211> 891
<212> DNA
<213> Pantoea stewartii

<220>
<221> CDS
<222> (1)..(891)

<400> 9
atg gcg gtt ggc tcg aaa agc ttt gcg act gca tcg acg ctt ttc gac 48
Met Ala Val Gly Ser Lys Ser Phe Ala Thr Ala Ser Thr Leu Phe Asp
1 5 10 15

gcc aaa acc cgt cgc agc gtg ctg atg ctt tac gca tgg tgc cgc cac 96
Ala Lys Thr Arg Arg Ser Val Leu Met Leu Tyr Ala Trp Cys Arg His
20 25 30

tgc gac gac gtc att gac gat caa aca ctg ggc ttt cat gcc gac cag 144
Cys Asp Asp Val Ile Asp Asp Gln Thr Leu Gly Phe His Ala Asp Gln
35 40 45

ccc tct tcg cag atg cct gag cag cgc ctg cag cag ctt gaa atg aaa 192
Pro Ser Ser Gln Met Pro Glu Gln Arg Leu Gln Gln Leu Glu Met Lys

```
    50                  55                  60

acg cgt cag gcc tac gcc ggt tcg caa atg cac gag ccc gct ttt gcc      240
Thr Arg Gln Ala Tyr Ala Gly Ser Gln Met His Glu Pro Ala Phe Ala
65                  70                  75                  80

gcg ttt cag gag gtc gcg atg gcg cat gat atc gct ccc gcc tac gcg      288
Ala Phe Gln Glu Val Ala Met Ala His Asp Ile Ala Pro Ala Tyr Ala
                85                  90                  95

ttc gac cat ctg gaa ggt ttt gcc atg gat gtg cgc gaa acg cgc tac      336
Phe Asp His Leu Glu Gly Phe Ala Met Asp Val Arg Glu Thr Arg Tyr
            100                 105                 110

ctg aca ctg gac gat acg ctg cgt tat tgc tat cac gtc gcc ggt gtt      384
Leu Thr Leu Asp Asp Thr Leu Arg Tyr Cys Tyr His Val Ala Gly Val
        115                 120                 125

gtg ggc ctg atg atg gcg caa att atg ggc gtt cgc gat aac gcc acg      432
Val Gly Leu Met Met Ala Gln Ile Met Gly Val Arg Asp Asn Ala Thr
    130                 135                 140

ctc gat cgc gcc tgc gat ctc ggg ctg gct ttc cag ttg acc aac att      480
Leu Asp Arg Ala Cys Asp Leu Gly Leu Ala Phe Gln Leu Thr Asn Ile
145                 150                 155                 160

gcg cgt gat att gtc gac gat gct cag gtg ggc cgc tgt tat ctg cct      528
Ala Arg Asp Ile Val Asp Asp Ala Gln Val Gly Arg Cys Tyr Leu Pro
                165                 170                 175

gaa agc tgg ctg gaa gag gaa gga ctg acg aaa gcg aat tat gct gcg      576
Glu Ser Trp Leu Glu Glu Glu Gly Leu Thr Lys Ala Asn Tyr Ala Ala
            180                 185                 190

cca gaa aac cgg cag gcc tta agc cgt atc gcc ggg cga ctg gta cgg      624
Pro Glu Asn Arg Gln Ala Leu Ser Arg Ile Ala Gly Arg Leu Val Arg
        195                 200                 205

gaa gcg gaa ccc tat tac gta tca tca atg gcc ggt ctg gca caa tta      672
Glu Ala Glu Pro Tyr Tyr Val Ser Ser Met Ala Gly Leu Ala Gln Leu
    210                 215                 220

ccc tta cgc tcg gcc tgg gcc atc gcg aca gcg aag cag gtg tac cgt      720
Pro Leu Arg Ser Ala Trp Ala Ile Ala Thr Ala Lys Gln Val Tyr Arg
225                 230                 235                 240

aaa att ggc gtg aaa gtt gaa cag gcc ggt aag cag gcc tgg gat cat      768
Lys Ile Gly Val Lys Val Glu Gln Ala Gly Lys Gln Ala Trp Asp His
                245                 250                 255

cgc cag tcc acg tcc acc gcc gaa aaa tta acg ctt ttg ctg acg gca      816
Arg Gln Ser Thr Ser Thr Ala Glu Lys Leu Thr Leu Leu Leu Thr Ala
            260                 265                 270

tcc ggt cag gca gtt act tcc cgg atg aag acg tat cca ccc cgt cct      864
Ser Gly Gln Ala Val Thr Ser Arg Met Lys Thr Tyr Pro Pro Arg Pro
        275                 280                 285

gct cat ctc tgg cag cgc ccg atc tag                                  891
Ala His Leu Trp Gln Arg Pro Ile
    290                 295
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<210> 10
<211> 296
<212> PRT
<213> Pantoea stewartii

<400> 10

Met Ala Val Gly Ser Lys Ser Phe Ala Thr Ala Ser Thr Leu Phe Asp
1 5 10 15

Ala Lys Thr Arg Arg Ser Val Leu Met Leu Tyr Ala Trp Cys Arg His
20 25 30

Cys Asp Asp Val Ile Asp Asp Gln Thr Leu Gly Phe His Ala Asp Gln
35 40 45

Pro Ser Ser Gln Met Pro Glu Gln Arg Leu Gln Gln Leu Glu Met Lys
50 55 60

Thr Arg Gln Ala Tyr Ala Gly Ser Gln Met His Glu Pro Ala Phe Ala
65 70 75 80

Ala Phe Gln Glu Val Ala Met Ala His Asp Ile Ala Pro Ala Tyr Ala
85 90 95

Phe Asp His Leu Glu Gly Phe Ala Met Asp Val Arg Glu Thr Arg Tyr
100 105 110

Leu Thr Leu Asp Asp Thr Leu Arg Tyr Cys Tyr His Val Ala Gly Val
115 120 125

Val Gly Leu Met Met Ala Gln Ile Met Gly Val Arg Asp Asn Ala Thr
130 135 140

Leu Asp Arg Ala Cys Asp Leu Gly Leu Ala Phe Gln Leu Thr Asn Ile
145 150 155 160

Ala Arg Asp Ile Val Asp Asp Ala Gln Val Gly Arg Cys Tyr Leu Pro
165 170 175

Glu Ser Trp Leu Glu Glu Glu Gly Leu Thr Lys Ala Asn Tyr Ala Ala
180 185 190

Pro Glu Asn Arg Gln Ala Leu Ser Arg Ile Ala Gly Arg Leu Val Arg
195 200 205

Glu Ala Glu Pro Tyr Tyr Val Ser Ser Met Ala Gly Leu Ala Gln Leu
210 215 220

Pro Leu Arg Ser Ala Trp Ala Ile Ala Thr Ala Lys Gln Val Tyr Arg
225 230 235 240

Lys Ile Gly Val Lys Val Glu Gln Ala Gly Lys Gln Ala Trp Asp His
245 250 255

Arg Gln Ser Thr Ser Thr Ala Glu Lys Leu Thr Leu Leu Leu Thr Ala
260 265 270

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Ser Gly Gln Ala Val Thr Ser Arg Met Lys Thr Tyr Pro Pro Arg Pro
        275                 280                 285

Ala His Leu Trp Gln Arg Pro Ile
    290                 295
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<210> 11
<211> 528
<212> DNA
<213> Pantoea stewartii

<220>
<221> CDS
<222> (1)..(528)

<400> 11

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atg ttg tgg att tgg aat gcc ctg atc gtg ttt gtc acc gtg gtc ggc       48
Met Leu Trp Ile Trp Asn Ala Leu Ile Val Phe Val Thr Val Val Gly
1               5                   10                  15

atg gaa gtg gtt gct gca ctg gca cat aaa tac atc atg cac ggc tgg       96
Met Glu Val Val Ala Ala Leu Ala His Lys Tyr Ile Met His Gly Trp
            20                  25                  30

ggt tgg ggc tgg cat ctt tca cat cat gaa ccg cgt aaa ggc gca ttt      144
Gly Trp Gly Trp His Leu Ser His His Glu Pro Arg Lys Gly Ala Phe
        35                  40                  45

gaa gtt aac gat ctc tat gcc gtg gta ttc gcc att gtg tcg att gcc      192
Glu Val Asn Asp Leu Tyr Ala Val Val Phe Ala Ile Val Ser Ile Ala
    50                  55                  60

ctg att tac ttc ggc agt aca gga atc tgg ccg ctc cag tgg att ggt      240
Leu Ile Tyr Phe Gly Ser Thr Gly Ile Trp Pro Leu Gln Trp Ile Gly
65                  70                  75                  80

gca ggc atg acc gct tat ggt tta ctg tat ttt atg gtc cac gac gga      288
Ala Gly Met Thr Ala Tyr Gly Leu Leu Tyr Phe Met Val His Asp Gly
                85                  90                  95

ctg gta cac cag cgc tgg ccg ttc cgc tac ata ccg cgc aaa ggc tac      336
Leu Val His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr
            100                 105                 110

ctg aaa cgg tta tac atg gcc cac cgt atg cat cat gct gta agg gga      384
Leu Lys Arg Leu Tyr Met Ala His Arg Met His His Ala Val Arg Gly
        115                 120                 125

aaa gag ggc tgc gtg tcc ttt ggt ttt ctg tac gcg cca ccg tta tct      432
Lys Glu Gly Cys Val Ser Phe Gly Phe Leu Tyr Ala Pro Pro Leu Ser
    130                 135                 140

aaa ctt cag gcg acg ctg aga gaa agg cat gcg gct aga tcg ggc gct      480
Lys Leu Gln Ala Thr Leu Arg Glu Arg His Ala Ala Arg Ser Gly Ala
145                 150                 155                 160

gcc aga gat gag cag gac ggg gtg gat acg tct tca tcc ggg aag taa      528
Ala Arg Asp Glu Gln Asp Gly Val Asp Thr Ser Ser Ser Gly Lys
                165                 170                 175
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<210> 12
<211> 175

<212> PRT
<213> Pantoea stewartii

<400> 12

Met Leu Trp Ile Trp Asn Ala Leu Ile Val Phe Val Thr Val Val Gly
1 5 10 15

Met Glu Val Val Ala Ala Leu Ala His Lys Tyr Ile Met His Gly Trp
20 25 30

Gly Trp Gly Trp His Leu Ser His His Glu Pro Arg Lys Gly Ala Phe
35 40 45

Glu Val Asn Asp Leu Tyr Ala Val Val Phe Ala Ile Val Ser Ile Ala
50 55 60

Leu Ile Tyr Phe Gly Ser Thr Gly Ile Trp Pro Leu Gln Trp Ile Gly
65 70 75 80

Ala Gly Met Thr Ala Tyr Gly Leu Leu Tyr Phe Met Val His Asp Gly
85 90 95

Leu Val His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr
100 105 110

Leu Lys Arg Leu Tyr Met Ala His Arg Met His His Ala Val Arg Gly
115 120 125

Lys Glu Gly Cys Val Ser Phe Gly Phe Leu Tyr Ala Pro Pro Leu Ser
130 135 140

Lys Leu Gln Ala Thr Leu Arg Glu Arg His Ala Ala Arg Ser Gly Ala
145 150 155 160

Ala Arg Asp Glu Gln Asp Gly Val Asp Thr Ser Ser Ser Gly Lys
165 170 175

<210> 13
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> First primer used to amplify carotenoid gene cluster.

<400> 13
atgacggtct gcgcaaaaaa acacg 25

<210> 14
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Second primer used to amplify carotenoid gene cluster.

<400> 14
gagaaattat gttgtggatt tggaatgc 28

<210> 15
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Primer Tn5PCRF.

<400> 15
gctgagttga aggatcagat c 21

<210> 16
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Primer Tn5PCRR.

<400> 16
cgagcaagac gtttcccgtt g 21

<210> 17
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> Primer Kan-2 FP-1

<400> 17
acctacaaca aagctctcat caacc 25

<210> 18
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> Primer Kan-2 RP-1

<400> 18
gcaatgtaac atcagagatt ttgag 25

<210> 19
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Primer Y1_F

<400> 19
agcaccatga tcatctggcg 20

<210> 20
<211> 20
<212> DNA

<213> Artificial sequence

<220>
<223> Primer Y1_R

<400> 20
cggttgcgct ggaagaaaac 20

<210> 21
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Primer Y4_F

<400> 21
caccctgtgc cattttcagc 20

<210> 22
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Primer Y4_R

<400> 22
cgttctgggt atggcccaga 20

<210> 23
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Primer Y8_1_F

<400> 23
aaagctaacc cgtggcagca 20

<210> 24
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Primer Y8_1_R

<400> 24
tttgcgttcc ccgaggcata 20

<210> 25
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Primer Y12_F

<400> 25
ttccgaaatg gcgtcagctc 20

<210> 26
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> Primer Y12_R

<400> 26
atctctacat tgattatgag tattc 25

<210> 27
<211> 20
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<220>
<223> Primer Y15_F

<400> 27
ggatcgatct tgagatgacc 20

<210> 28
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Primer Y15_R

<400> 28
gctttcgtaa ttttcgcatt tctg 24

<210> 29
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Primer Y16_F

<400> 29
cacgccaagt tgcgcaagta 20

<210> 30
<211> 20
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<220>
<223> Primer Y16_R

<400> 30
gcagaaaatg gtgactcagg 20

<210> 31
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<220>
<223> Primer Y17_F

<400> 31
ggcgatcctc gtcgatttct 20

<210> 32
<211> 20
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<220>
<223> Primer Y17_R

<400> 32
acgcagacga gagtttgcgt 20

<210> 33
<211> 20
<212> DNA
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<220>
<223> Primer Y21_F

<400> 33
accgaatgcc cttgctgttg 20

<210> 34
<211> 20
<212> DNA
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<220>
<223> Primer Y21_R

<400> 34
gggtgttcag gtatggctta 20

<210> 35
<211> 3159
<212> DNA
<213> Escherichia coli

<400> 35
atgcctgtta taactcttcc tgatggcagc caacgccatt acgatcacgc tgtaagcccc 60

atggatgttg cgctggacat tggtccaggt ctggcgaaag cctgtatcgc agggcgcgtt 120

aatggcgaac tggttgatgc ttgcgatctg attgaaaacg acgcacaact gtcgatcatt 180

accgccaaag acgaagaagg tctggagatc attcgtcact cctgtgcgca cctgttaggg 240

cacgcgatta aacaactttg gccgcatacc aaaatggcaa tcggcccggt tattgacaac 300

ggtttttatt acgacgttga tcttgaccgc acgttaaccc aggaagatgt cgaagcactc 360

gagaagcgga tgcatgagct tgctgagaaa aactacgacg tcattaagaa gaaagtcagc 420

tggcacgaag cgcgtgaaac tttcgccaac cgtggggaga gctacaaagt ctccattctt 480

gacgaaaaca tcgcccatga tgacaagcca ggtctgtact tccatgaaga atatgtcgat 540

atgtgccgcg gtccgcacgt accgaacatg cgtttctgcc atcatttcaa actaatgaaa 600

acggcagggg cttactggcg tggcgacagc aacaacaaaa tgttgcaacg tatttacggt 660

acggcgtggg cagacaaaaa agcacttaac gcttacctgc agcgcctgga agaagccgcg 720
aaacgcgacc accgtaaaat cggtaaacag ctcgacctgt accatatgca ggaagaagcg 780
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tccaacatgg atgctgattt atatgggtat aaatgggctc gcgataatgt cgggcaatca 2160
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gttggacgag tcggaatcgc agaccgatac caggatcttg ccatcctatg gaactgcctc 2760

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gatatgaata aattgcagtt tcatttgatg ctcgatgagt ttttctaatc agaattggtt 2880

aattggttgt aacactggca gagcattacg ctgacttgac gggacggcgg ctttgttgaa 2940

taaatcgaac ttttgctgag ttgaaggatc agatcacgca tcttcccgac aacgcagacc 3000

gttccgtggc aaagcaaaag ttcaaaatca ccaactggtc cacctacaac aaagctctca 3060

tcaaccgtgg cggggatcct ctagagtcga cctgcaggca tgcaagcttc agggttgaga 3120

tgtgtataag agacaggtct taaacaattg gaggaataa 3159

<210> 36
<211> 3171
<212> DNA
<213> Escherichia coli

<400> 36
atgatgagtt atgtagactg gccgccatta attttgaggc acacgtacta catggctgaa 60

ttcgaaacca cttttgcaga tctgggcctg aaggctccta tccttgaagc ccttaacgat 120

ctgggttacg aaaaaccatc tccaattcag gcagagtgta ttccacatct gctgaatggc 180

cgcgacgttc tgggtatggc ccagacgggg agcggaaaaa ctgcagcatt ctctttacct 240

ctgttgcaga atcttgatcc tgagctgaaa gcaccacaga ttctggtgct ggcaccgacc 300

cgcgaactgg cggtacaggt tgctgaagca atgacggatt tctctaaaca catgcgcggc 360

gtaaatgtgg ttgctctgta cggcggccag cgttatgacg tgcaattacg cgccctgcgt 420

caggggccgc agatcgttgt cggtactccg ggccgtctgc tggaccacct gaaacgtggc 480

actctggacc tctctaaact gagcggtctg gttctggatg aagctgacga aatgctgcgc 540

atgggcttca tcgaagacgt tgaaaccatt atggcgcaga tcccggaagg tcatcagacc 600

gctctgttct ctgcaaccat gccggaagcg attcgtcgca ttacccgccg ctttatgaaa 660

gagccgcagg aagtgcgcat tcagtccagc gtgactaccc gtcctgacat cagccagagc 720

tactggactg tctggggtat gcgcaaaaac gaagcactgg tacgctgtct cttatacaca 780

tctcaaccat catcgatgaa ttgtgtctca aaatctctga tgttacattg cacaagataa 840

aaatatatca tcatgaacaa taaaactgtc tgcttacata aacagtaata caaggggtgt 900

tatgagccat attcaacggg aaacgtcttg ctcgaggccg cgattaaatt ccaacatgga 960

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